REMARKS

Entry of the above amendment prior to examination is respectfully requested.

Attached hereto is a marked-up version of the changes made to the specification and claims by the current amendment. The attached page(s) is/are captioned **"Version with Markings to Show Changes Made."**

I. Amendments

The Sequence Listing has been amended in accordance with 37 C.F.R. §1.821 to include unbranched nucleotide sequences with ten or more nucleotides.

The specification has been amended in accordance with 37 C.F.R. §1.821(d) to add sequence identifiers

If in the opinion of the Examiner a telephone conference would expedite the prosecution of the subject application, the Examiner is encouraged to call the undersigned at (650) 838-4410.

Respectfully submitted,

Jacqueline F. Mahoney

Date: May 1, 2002

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the following, added portions are indicated by **underlining and boldface**, to avoid confusion with portions underlined in the original text.

On page 7, please replace the paragraph starting on line 5 with the following:

-- Figure 1A presents the sequence of the HBV core promoter **(SEQ ID NO:16)**.--

On page 7, please replace the paragraph starting on line 6 with the following:

-- Figure 1B presents the sequence of the HBV pre-S1 promoter region **(SEQ ID NO:22)** with the sequences of various DNA response elements (HNF1, HNF3, Sp1 and TBP) indicated as underlined with sequence locations indicated in the figure.--

On page 7, please replace the paragraph starting on line 9 with the following:

-- Figure 2 depicts the results of a hybridization stabilization assay (HSA) with various HBV preS1 promoter constructs **(SEQ ID NO:246-250)** indicating the binding preference of a test compound, the netropsin dimer, 21x, for the HNF3-wt, TBP-wt, TBP-mut, HNF-1-wt, HNF1-m and HNF1-21x sequences, indicated in the figure.--

On page 7, please replace the paragraph starting on line 13 with the following:

-- Figure 3 presents the sequence of the HBV X promoter region **(SEQ ID NO:25)** with the sequences of various DNA response elements (NF1, 2c, EF-C, NF-1 and X-PBP) indicated as underlined in the figure.--

On page 7, please replace the paragraph starting on line 16 with the following:

-- Figure 4 presents the sequence of the wild type cyclin D1 promoter **(SEQ ID NO:1)** from -1745 to +155, which corresponds to nucleotides 316 to 2161 of GenBank Accession No. L09054.--

On page 7, please replace the paragraph starting on line 18 with the following:

-- Figures 5A to C present the sequence of the full-length human CD40L sequence **(SEQ ID NO:9)** numbered from nucleotide 1 to 2395, wherein nucleotides 10 to 1919 correspond to the human CD40L promoter sequence identified as -1860 to +49.--

On page 7, please replace the paragraph starting on line 21 with the following:

-- Figure 6 presents the sequence of the wild type vanH promoter **(SEQ ID NO:31)**.--

On page 7, please replace the paragraph starting on line 22 with the following:

-- Figure 7 presents the sequences of vanH promoter mutants M2-M21 **(SEQ ID NO:79 and 192-210)**, wherein each group of 10 nucleotides in the original vanH promoter sequence **(SEQ ID NO:31)** shown in the figure was replaced with the mutant sequence, *e.g.*, in M2 the CCCGGGGGGC **(SEQ ID NO:79)** sequence was inserted in place of the wild type TAATTTTTTA **(SEQ ID NO:80)** sequence.--

On page 7, please replace the paragraph starting on line 26 with the following:

-- Figures 8A to C present the sequence of the wild type androgen receptor promoter **(SEQ ID NO:35)** from -6000 to +1100.--

On page 7, please replace the paragraph starting on line 28 with the following:

-- Figure 9 presents the sequence of the wild type Her2 promoter **(SEQ ID NO:67)**.--

On page 16, please replace the paragraph starting on line 26 with the following:

-- In one example involving the cyclin D1 promoter, the hybridization stabilization assay employs a 12bp DNA duplex as an indicator for binding, wherein one strand of the duplex (CTTTATTATTTT**, SEQ ID NO:81**) is 5' labeled with fluorescein, and the complementary strand is 5' labeled with a dabsyl quenching molecule (AAAATAATAAAG-3'**, SEQ ID NO:82**). When the two strands are mixed together with a DNA-binding molecule, which can stabilize the duplex form, the signal from the fluorescein is quenched by the dabsyl on the complementary strand. Various cold competitor duplexes can then be added to see whether they provide preferred binding sites for the DNA-binding compound. If the competitor DNA, binds the DNA-binding molecule, the DNA-binding molecule is titrated away from the indicator duplex resulting in destabilization of the indicator duplex and as the strands separate, quenching is diminished and fluorescence increases.--

On page 33, please replace the paragraph starting on line 5 with the following:

-- Mutation of the E2F site {Motokura & Arnold, 1993} resulted in a construct which retained 63% of wild-type activity. Mutation of the CRE element resulted in a construct that retained 32% of wild-type activity, indicating that it is important to basal cyclin D1 expression in MCF7 cells.

-60 -37

AACAACAGTAACGTCACACGGACT **(SEQ ID NO:83)**

TTGTTGTCATTGCAGTGTGCCTGA

CRE --

On page 36, please replace Table 3 with the following:

--Table 3. Reporter Activity of Cyclin D1 Promoter Constructs

Mutant Construct	Mutant Sequence	Wild Type Sequence	% Wild Type Activity
mAP1	AAAAAAAATACGCGTGAATGGA **(SEQ ID NO:84)**	AAAAAAAATGAGTCAGAATGGA **(SEQ ID NO:92)**	111 +/- 12.8
mAP1ds	TCACCAGTTCTTGGACTGT **(SEQ ID NO:85)**	TCAGAATGGAGATCACTGT **(SEQ ID NO:93)**	79 +/- 8.4
mE2F	GGAATTGGATCCCATTT **(SEQ ID NO:86)**	GGAATTTTCGGGCATTT **(SEQ ID NO:94)**	63 +/- 10.5
mOCT1	GGGGCGGGATCCTTCT **(SEQ ID NO:87)**	GGGGCGATTTGCTTCT **(SEQ ID NO:95)**	92 +/- 7.7
mSP1	TGCGCTTTTAATTAAAACCCT **(SEQ ID NO:88)**	TGCGCCCGCCCCCGCCCCCCCT **(SEQ ID NO:96)**	105 +/- 5.6
CREbam	CAGTGGATCCACACGG **(SEQ ID NO:89)**	CAGTAACGTCACACGG **(SEQ ID NO:7)**	32 +/- 1.7
CRE4C	CAGTAAGGTCACACGG **(SEQ ID NO:90)**	CAGTAACGTCACACGG **(SEQ ID NO:7)**	33 +/- 5.0
CRE4C5G	CAGTAAGCTCACACGG **(SEQ ID NO:91)**	CAGTAACGTCACACGG **(SEQ ID NO:7)**	33 +/- 5.0

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On page 36, please replace Table 4 with the following:

--Table 4 Reporter Activity of Cyclin D1 Promoter Constructs

Construct	Mutations in –30-21 region	% Wild Type Activity
WT/-1745	GAGTTTTGTT **(SEQ ID NO:5)**	100
-30 -21/-1745	TCTGGGATCC **(SEQ ID NO:97)**	33 +/- 2.2
-30 -26/-1745	TCTGGTTGTT **(SEQ ID NO:98)**	43 +/- 3.5
-25 -21/-1745	GAGTTGGCGG **(SEQ ID NO:99)**	34 +/- 4.7
-30 -28/-1745	TCTTTTTGTT **(SEQ ID NO:100)**	33 +/- 6.3
-28 –23/-1745	GATGGGATTT **(SEQ ID NO:101)**	46 +/- 5.1
-23 -21/-1745	GAGTTTTTCC **(SEQ ID NO:102)**	138 +/- 16.4
10 bp 21x/-1745	GAGTTTTTTTTAAG **(SEQ ID NO:103)**	87 +/- 11.4
8 bp 21x /-1745	GAGTTTTAAAAGAG **(SEQ ID NO:104)**	85 +/- 7.8

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On page 41, please replace Table 8 with the following:

--Table 8 Site Specific Mutations and Promoter Activity

Mutation	Wild Type Sequence	% Wild Type Activity
-1194 NFkB	GGGATTTCC	83%
-760 NF-AT	TTTTCC	91%
-599 NF-AT	GGAAAA	100% +/- 0%
-306	TTGTCACTTTC **(SEQ ID NO:105)**	24% +/- 4%
-269 GATA-3	GTGATA	67%
-264 NF-AT	GGAAAA	73% +/- 25%
-66 NF-AT	TTTTCC	32% +/- 4%
-37 to -29 TFIIB	GTGCGCT	53% +/- 19%
-30 to -25 TATA	CTTAAC	47% +/- 12%
-220 to -214	GGCAAG	26% +/- 3.5%
-214 to -208	AATGAA	31% +/- 6.9%
-208 to -202	TATATG	38% +/- 9.9%
-202 to -196	GAAGAA	36% +/- 4
-220 to -208	GGCAAGAATGAA **(SEQ ID NO:106)**	18% +/- 2.6
-72 to -66	AGCACA	49% +/- 48%
-66 to -60	TTTTCC	31% +/- 5.8
-60 to -54	AGGAAG	42%+/- 2
-54 to -48	TGTGGG	19% +/- 3.8
-48 to -42	CTGCAA	50% +/- 6%
-72 to -60	AGCACATTTTCC **(SEQ ID NO:107)**	10% +/- 1.8%
-66 to -54	TTTTCCAGGAAG **(SEQ ID NO:108)**	7% +/- 1.8%
-66 to -60 and -54 to -48	TTTTCC TGTGGG **(SEQ ID NO:109)**	14% +/- 2.2%
-66 to -60 and -48 to -42	TTTTCC CTGCAA **(SEQ ID NO:110)**	15%
-54 to -42	TGTGGCTGCAA **(SEQ ID NO:111)**	20% +/- 5.5%
-66 to -48	TTTTCCAGGAAGTGTGGG **(SEQ ID NO:112)**	11% +/- 1.5%
-72 to -60 and -54 to -48	AGCACATTTTCC TGTGGG **(SEQ ID NO:113)**	8% +/- 1.4%
-66 to -60 and -54 to -42	TTTTCC TGTGGGCTGCAA **(SEQ ID NO:114)**	5% +/- 15%

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On page 43, please replace Table 9 with the following:

--Table 9 Reporter Analysis of Linker Scanner Mutation Clones of the HBV Core Promoter

Domain	Nucleotide Coordinates[2]	Linker Scanner Sequence	Wild Type Sequence	Percent Wild Type	
1	1601 – 1615	ACATGATATCTTCT **SEQ ID NO:115)**	GCACGTCGCATGGAG **(SEQ ID NO:129)**	HepG2	HepAD38
2	1616 – 1630	AAGAATTCCCATAA **SEQ ID NO:116)**	ACCACCGTGAACGCC **(SEQ ID NO:130)**	88	147
3	1631 – 1645	CAACCCGCGGTAAA **SEQ ID NO:117)**	CACCAAATATTGCCC **(SEQ ID NO:131)**	79	65
4	1646 – 1660	CTTGAGGCACGCGT **SEQ ID NO:118)**	AAGGTCTTACATAAG **(SEQ ID NO:132)**	28	38
5-1	1661 – 1668	TCTAGAG	AGGACTCT	34	10
5-2	1668 – 1675	GTCTAGA	TTGGACTC	22	18
6	1676 – 1690	ACGTCCGTGACCAT **SEQ ID NO:119)**	TCAGCAATGTCAACG **(SEQ ID NO:133)**	91	128
7	1691 – 1705	AATCAAGATCTTAC **SEQ ID NO:120)**	ACCGACCTTGAGGCA **(SEQ ID NO:134)**	76	93
8	1706 – 1720	CAGGACCCTCGAGG **SEQ ID NO:121)**	TACTTCAAAGACTGT **(SEQ ID NO:19)**	7	9
9-1	1721 – 1728	GTGCACC	TTGTTTAA	14	11
9-2	1728 – 1735	TAGTGTT	AAGACTGG	24	17
10	1736 – 1750	CTTCTAGATTTTCT **SEQ ID NO:122)**	GAGGAGTTGGGGGAG **(SEQ ID NO:135)**	22	22
11	1751 – 1765	CTCGGCTTGGCCAT **SEQ ID NO:123)**	GAGATTAGGTTAAAG **(SEQ ID NO:136)**	24	26
12-1	1766 – 1773	GCGCATG	GTCTTTGT	103	103
12-2	1771 – 1780	TGCACCTTC **SEQ ID NO:124)**	TGTACTAGGA **(SEQ ID NO:137)**	37	36
13	1781 – 1795	TAGTGCTTAAGCCC **SEQ ID NO:125)**	GGCTGTAGGCATAAA **(SEQ ID NO:21)**	16	14
14	1796 – 1810	CTCGAGTATACAAC **SEQ ID NO:126)**	TTGGTCTGCGCACCA **(SEQ ID NO:138)**	37	68
15	1811 – 1825	ACAACGTACCCGGG **SEQ ID NO:127)**	GCACCATGCAACTTT **(SEQ ID NO:139)**	129	185
16	1826 – 1840	GACAAGCTTAAGCC **SEQ ID NO:128)**	TTCACCTCTGCCTAA **(SEQ ID NO:140)**	229	247

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On page 44, please replace Table 10 with the following:

--Table 10 Reporter Analysis of Site-Directed Mutants of HNF3 and HNF4 Sites of the HBV Core Promoter

	Nucleotide Coordinates (HBV ayw Strain)	Site-Directed Mutant Sequence	Percent Wild Type HepAD38
Distal HNF3	1680 – 1691	CCAGGGCCCCGA **(SEQ ID NO:141)**	102
Proximal HNF3	1715 – 1726	GCCGCGGTCTGT **(SEQ ID NO:142)**	33
HNF4	1661 – 1672	CGTCCGCGGTGA **(SEQ ID NO:143)**	29

[2] HBV ayw strain

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On page 45, please replace Table 11 with the following:

--Table 11. PreS1 Promoter Activity of Mutants

Construct	Coordinate	Mutated Sequence	% Wild type Activity
HNF1	2720-2732	5' TCGCGAACGGCAG **(SEQ ID NO:144)**	6
HNF3	2744-2755	5' ACAGCGCGCACA **(SEQ ID NO:145)**	40
Sp1	2765-2774	5' CGATATCTGC **(SEQ ID NO:146)**	48
TBP	2778-2784	5' GCGCGCC	34
Domain 1	2702-2716	5' GCGGCGAACTGCACG **(SEQ ID NO:147)**	182
Domain 2	2717-2731	5' AGCCGCGGGACGGCA **(SEQ ID NO:148)**	8
Domain 3	2732-2746	5' GGAACCCAGCTGACA **(SEQ ID NO:149)**	62
Domain 4	2747-2761	5' GCGCGCACACAGAGC **(SEQ ID NO:150)**	103
Domain 5	2762-2776	5' GTCTGCAGTTTGCGC **(SEQ ID NO:151)**	115
Domain 6	2777-2791	5' GGCGCGCCTCTCTCC **(SEQ ID NO:152)**	34
Domain 7	2792-2806	5'CAGCTGACGCTATAA **(SEQ ID NO:153)**	53
Domain 8	2807-2821	5'GACGGGCCCTTTGAG **(SEQ ID NO:154)**	55

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On page 45, please replace Table 12 with the following:

--Table 12. HNF1 Linker-Scanning Mutagenesis

Construct	HNF1 sequence	% Wild type Activity
Wild type	GTTAATCATTACT **(SEQ ID NO:155)**	100
HNF1-A	TCGCATCATTAC **(SEQ ID NO:156)**	4
HNF1-B	GTTCCGAATTAC **(SEQ ID NO:157)**	3
HNF1-C	GTTAATACGGAC **(SEQ ID NO:158)**	4
HNF1-D	GTTAATCATGCAG **(SEQ ID NO:159)**	5

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On page 46, please replace Table 13 with the following:

--Table 13. Mutants In The HNF1 Site Of The PreS1 Promoter

Consensus sequence	***GTT AAT NAT TAA C* (SEQ ID NO:160)**	**Relative Luciferase Activity (%)**		
Wild type	GTT AAT CAT TAC TT **(SEQ ID NO:161)**	100	100	100
mHNF1	TCG CAG ACG GCA GT **(SEQ ID NO:162)**	5	5	5
HNF1-4A	GTT GAT CAT TAC TT **(SEQ ID NO:163)**	-	5	-
HNF1-5A	GTT ACT CAT TAC TT **(SEQ ID NO:164)**	42	30	
HNF1-5B	GTT AGT CAT TAC TT **(SEQ ID NO:165)**	20	-	-
HNF1-6A	GTT AAG CAT TAC TT **(SEQ ID NO:166)**	-	6	-
HNF1-6B	GTT AAC CAT TAC TT **(SEQ ID NO:167)**	29	-	-
HNF1-9A	GTT AAT CAG TAC TT **(SEQ ID NO:168)**	-	3	-
HNF1-9B	GTT AAT CAC TAC TT **(SEQ ID NO:169)**	14	-	-
HNF1-5A6B	GTT ACC CAT TAC TT **(SEQ ID NO:170)**	-	-	9
HNF1-5A9B	GTT ACT CAC TAC TT **(SEQ ID NO:171)**	-	-	4

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On page 48, please replace Table 14 with the following:

--Table 14. Linker Scanning Mutants of X Promoter

Construct	Coordinate	Mutated Sequence	% Wild Type Activity (HepG2)	% Wild Type Activity (2.2.15)	% Wild -Type Activity (HepAD38)
Domain 1	1083-1103	5' CCTACTTCGCGACAGGGAGAT **(SEQ ID NO:172)**	10(343/103)	172/75	230/100
Domain 2	1104-1124	5' AACCAGGGCCCTTATGGGAGT **(SEQ ID NO:173)**	95/98	69	58
Domain 3	1125-1145	5' GTGCCCATCGCGAGTCCAAGG **(SEQ ID NO:174)**	33/38	51	40
Domain 4	1146-1166	5' GCAAAATGGGATATCACCATT **(SEQ ID NO:175)**	59/36	51	45
Domain 5	1167-1187	5' AACTGCAGTGTAACCTGTGGG **(SEQ ID NO:176)**	113/105	83	119
Domain 6	1188-1208	5' TACAGATATCAAAAACAGTTA **(SEQ ID NO:177)**	33/40	28	33
Domain 7	1209-1229	5' GTTTTAGGATATCGTTTAACG **(SEQ ID NO:178)**	81/85	71	66
Domain 8	1230-1250	5' ACTATACGGATATCCCAAGGG **(SEQ ID NO:179)**	41/47	64	47
Domain 9	1251-1271	5' GATTACAAGAGATATCGAACG **(SEQ ID NO:180)**	48(56/39)	80/49	72/32
Domain 10	1272-1292	5' CAGTATTCCAGAAGATATCAG **(SEQ ID NO:181)**	51/50	62	70
Domain 11	1293-1313	5' GTGGGGAAGATATCACTTGAG **(SEQ ID NO:182)**	117/168	124	152
Domain 12	1314-1334	5' TTCTACCCACGGCGATATCAG **(SEQ ID NO:183)**	128	--	--
Domain 23	1335-1355	5' TCGCCAGAGTCGCGAAGCGAA **(SEQ ID NO:184)**	102/100	110	85

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On page 49, please replace Table 16 with the following:

--Table 16. Mutants of transcription factor binding sites of X Promoter

Domain	Coordinate	Mutated Sequence	WT Activity (HepG2)	% WT Activity (2.2.15)	% WT Activity (Hep AD38)
NF1	1100-1119	CTCGCCAACTTACAAGGCCT **(SEQ ID NO:185)**	109/109	119	93
2C	1119-1134	TTTCTGTGTAAACAAT **(SEQ ID NO:186)**	97/89	74	56
EF-C	1148-1168	CCCCGTTGCCCGGCAACGGCC **(SEQ ID NO:187)**	46/44	36	28
E	1180-1202	CTGACGCAACCCCC **(SEQ ID NO:188)**	47/39	53	39

NF1	1209-1229	TGGGGCTTGGTCATGGGCCA **(SEQ ID NO:189)**	88/95	80	78
NF1	1216-1236	TGGTCATGGGCCATCAGCGC **(SEQ ID NO:190)**	74/77	110	71
X-PBP	1229-1245	ATCAGCGCATGCGTGGAA **(SEQ ID NO:191)**	56/61	69	48

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On page 50, please replace the paragraph starting on line 13 with the following:

-- 20 linker scanning mutant designated M2-M21 were generated an nucleic acid constructs containing the VRE promoter sequence upstream of the luciferase gene were subcloned into the a pRLUC parent vector and transformed into *E. coli*. Figure 7 presents the sequences of vanH promoter mutants M2-M21, wherein each group of 10 nucleotides in the original vanH promoter sequence shown in the figure was replaced with the mutant sequence, *e.g.*, in M2 the CCCGGGGGGC sequence **(SEQ ID NO:79)** was inserted in place of the wild type TAATTTTTTA sequence **(SEQ ID NO:80)**. The position of the mutations and corresponding luciferase activity is shown in Table 18.--

On page 51, please replace Table 18 with the following:

--Table 18. vanH Promoter Mutants And Reporter Activity

Construct	Coordinate	Mutated Sequence	% Wild Type Activity (UCD3)	% Wild Type Activity (UL17)	% Wild Type Activity (CSUC4)
M2	-100 to -91	CCCGGGGGGC **(SEQ ID NO:79)**	120.4	53.6	10.7
M3	-90 to -81	TTCCCCGGGA **(SEQ ID NO:192)**	108.7	38.7	10.3
M4	-80 to -71	CCTAGGCGAG **(SEQ ID NO:193)**	--	--	0.4
M5	-70 to -61	GGCGCGCGGA **(SEQ ID NO:194)**	--	--	1.6
M6	-60 to -51	GCGCGCCCGG **(SEQ ID NO:195)**	36.5	10.3	0.4
M7	-50 to -41	CCACGCGCGC **(SEQ ID NO:196)**	45.5	18.9	1.8
M8	-40 to -31	GCGCGCTCCC **(SEQ ID NO:197)**	0.1	0.0	1.3
M9	-30 to -21	ATTGGTACCA **(SEQ ID NO:198)**	152.5	100.9	1202
M10	-20 to -11	GGCGCGCTGC **(SEQ ID NO:199)**	--	--	32.6
M11	-10 to -1	TCAGCGCGCA **(SEQ ID NO:200)**	1.3	--	1405
M12	+1 to +10	ATGCGCGCAT **(SEQ ID NO:201)**	--	--	1737
M13	+11 to +20	TTAACGGGGA	--	--	770.7

		(SEQ ID NO:202)			
M14	+21 to +30	TGGAGCGCGC **(SEQ ID NO:203)**	--	--	115.2
M15	+31 to +40	TCCGCGCGCT **(SEQ ID NO:204)**	--	--	50.6
M16	+41 to +50	CACGCGCGCA **(SEQ ID NO:205)**	--	--	23.6
M17	+51 to +60	ACGGAATTCA **(SEQ ID NO:206)**	--	--	2.4
M18	+61 to +70	AAAGCGCGCG **(SEQ ID NO:207)**	--	--	76.3
M19	+71 to +80	GGTACCAAGG **(SEQ ID NO:208)**	--	--	57.3
M20	+81 to +90	GACAGCTGCT **(SEQ ID NO:209)**	--	--	0.0
M21	+91 to +100	TTGGTTAACG **(SEQ ID NO:210)**	--	--	12.6

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On page 54, please replace Table 20 with the following:

--Table 20. Luciferase Reporter Activity of Various Her2 Promoter Constructs in MCF7 and ZR75 Cells

Construct	**Sequence (modification presented as underlined)**	**% Wild Type Activity (MCF7/ZR75)**
Her2 wild type	GAGCTGGGAGCGCGCTTGCTCCCAATCACCGGAGAAGGA **(SEQ ID NO:211)**	100/100
100 to 85	GA**TGGATCCTATATACC**GCTCCCAATCACCGGAGAAGGA **(SEQ ID NO:212)**	22/33
80 to 65	GAGCTGGGAGCGCGCTTGCTCC**AGGATCCATTCACCT**GA **(SEQ ID NO:213)**	30/29
90 to 75	GAGCTGGGAGCG**ATGGATCCAAACCGA**ACCGGAGAAGGA **(SEQ ID NO:214)**	9/12
87 to 79	GAGCTGGGAGCGCGC**GGATCCAAT**ATCACCGGAGAAGGA **(SEQ ID NO:215)**	16/12
84 to 76	GAGCTGGGAGCGCGCTTG**AGGATCCGA**ACCGGAGAAGGA **(SEQ ID NO:216)**	18/23
84 to 78	GAGCTGGGAGCGCGCTTT**AGATCT**ATCACCGGAGAAGGA **(SEQ ID NO:217)**	/17
81 to 76	GAGCTGGGAGCGCGCT**AAGCTT**CAATCACCGGAGAAGGA **(SEQ ID NO:218)**	/23
90 to 82	GAGCTGGGAGC**AATGGATCCA**CCAATCACCGGAGAAGGA **(SEQ ID NO:219)**	505/434
84 to 81	GAGCTGGGAGCGCGCTTT**AGA**CCAATCACCGGAGAAGGA **(SEQ ID NO:220)**	306/297
93 to 85	GAGCTGGGA**TAGGATCCT**CTCCCAATCACCGGAGAAGGA **(SEQ ID NO:221)**	41/62
81 to 73	GAGCTGGGAGCGCGCTTGCTC**AAGGATCCA**GAGGAAGGA **(SEQ ID NO:222)**	70/71
93 to 88	GAGC**GGATCC**CGCGCTTGCTCCCAATCACCGGAGAAGGA **(SEQ ID NO:223)**	/46
87 to 82	GAGCTGGGAG**GGATCC**TGCTCCCAATCACCGGAGAAGGA **(SEQ ID NO:224)**	/72
75 to 70	GAGCTGGGAGCGCGCTTGCTCC**AAGCTT**CCGGAGAAGGA **(SEQ ID NO:225)**	/132
75 to 70	GAGCTGGGAGCGCGCTTGCTCC**GGATCC**CCGGAGAAGGA **(SEQ ID NO:226)**	60/60

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On page 54, please replace the paragraph starting on line 13 with the following:

-- Mutations were made in various regions of the Her2 promoter, including an AT-rich region around and including a putative TATA box (TB, "TATAAGA"), a putative TATA box (T5B, CTTGAGGAAGGATCCGAATGAAGTTGT**, SEQ ID NO:227**), an AT stretch downstream of the putative TATA box (T3B, CTTGAGGAAGTATAATCCGGAAGTTGT**, SEQ ID NO:228**), a putative ets site (EP), a double mutant of the AT-rich region around and including the putative TATA box (TATA/Ets, CTTTCGATCGGATCCGCCGGAAGTTGT**, SEQ ID NO:229**), and the putative ets site (TBEP, "GAGGAA") as well as a deletion to -215. Sequence modifications are indicated as underlined.—

On page 55, please replace the paragraph starting on line 4 with the following:

-- The data suggest that sequences upstream of nucleotide –215 are not critical for regulation. As shown in Table 21, mutating the TATA box or the ets site causes a modest decrease in transcription, suggesting that a repressor site lies just downstream of the TATA box. The sequence near the putative TATA box and putative ets site is shown below.

CTGCTTGAGGAAGTATAAGAATGAAGTTGT **(SEQ ID NO:230)**

ets TATA box --

On page 57, please replace Table 24 with the following:

--Table 24. Sequences of Bla Promoter Mutants and Luciferase Reporter Activity

Mutants	Location	Wild Type Sequence	Mutated Sequence	Luciferase Activity (% Wild Type)
M6	-41 to -30	AATACATTCAAA **(SEQ ID NO:75)**	CCGGCCGGACCC **(SEQ ID NO:231)**	24%
M21	-35 to -30	TTCAAA	GGACCC	28%
M8	-17 to -6	CATGAGACAATA **(SEQ ID NO:76)**	ACGCGTCACCGC **(SEQ ID NO:232)**	29%
M30	-8 to -3	TAACC	CGCCAA	24%
M9	-5 to +7	ACCCTGATAAAT **(SEQ ID NO:77)**	CAAAGTCGACCG **(SEQ ID NO:233)**	15%
M11	+20 to +31	TTGAAAAAGGAA **(SEQ ID NO:78)**	GGGCCCCCTTCC **(SEQ ID NO:234)**	2%

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On page 58, please replace Table 25 with the following:

--Table 25. Sequences of pBlaMT and Mutant pBlaMT Constructs

Mutants	Sequence(-35 to +7 of BlaMT promoter)
PblaMT	TTCACACATGTATCCGCTCATGAGACAATAACCCTGATAAAT **(SEQ ID NO:235)**
pBlaMT(-35)	TTtAaAtATGTATCCGCTCATGAGACAATAACCCTGATAAAT **(SEQ ID NO:236)**
pBlaMT(-10)	TTCACACATGTATCCGCTCATGAGAtAATAAttCTGATAAAT **(SEQ ID NO:237)**
pBlaMT(-10p)	TTCACACATGTATCCGCTCATGAGACAATAACCCTGATgAAT **(SEQ ID NO:238)**
pBlaMT(-10/+1)	TTCACACATGTATCCGCTCATGAGACAATAAtttTGAcgAAT **(SEQ ID NO:239)**
pBlaMT (+1)	TTCACACATGTATCCGCTCATGAGACAATAACttTtATAAAT **(SEQ ID NO:240)**